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Nucleotide sequence coding for an outer membrane protein from *Neisseria meningitidis* and use of said protein in vaccine preparations

## **Abstract:**

The present invention is concerned with a method for the isolation of a nucleotide sequence which codes for a protein having a molecular weight of about 64 000 daltons, which is located on the outer membrane of *N. meningitidis*, as well as with the recombinant DNA obtained therefrom, which is used for the transformation of a host microorganism. The technical object pursued with the invention is the identification of a nucleotide sequence coding for a highly conserved and common protein for the majority of pathogenic *Neisseria* strains, the production of this protein with a high level of purity and in commercially useful amounts using the recombinant way, so that it can be used in diagnostic methods and vaccine preparations with a broad immunoprotection spectrum.

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(71) Applicant: **CENTRO DE INGENIERIA GENETICA  
Y BIOTECNOLOGIA  
31 Street, '156 & 190, Cubanacan Playa  
Havana(CU)**

(72) Inventor: **Rodriguez, Ricardo Silva  
Calle 15 No. 4209, entre 42 y 44, Playa  
La Habana(CU)**  
Inventor: **Houssein Sosa, Manuel Selman  
Paseo No. 126, entre 5ta y Calzada  
Vedado, La Habana(CU)**  
Inventor: **Nieto, Gerardo Guillén  
Linea No.6, Apto 4, entre N y O, Vedado  
La Habana(CU)**  
Inventor: **Herrera Martinez, Luis Saturnino  
Calle 96, entre 3a y 3aA, Playa  
La Habana(CU)**  
Inventor: **Fernández Mas , Julio Ra I  
Calle 26 No.873 1-2,Apto 3, entre Conill  
y45,Nuevo  
La Habana(CU)**  
Inventor: **Novoa Pérez, Lidia Inés  
Calle 184 No.3112, entre 31 y 33, Apto 49,  
Playa  
La Habana(CU)**  
Inventor: **Grillo, Juan Morales  
Compostela No.653, Apto 1, entre Luz y  
Acosta  
Habana Vieja, La Habana(CU)**  
Inventor: **Moreira Cordova, Vivian  
Calle 184 No.3112, entre 31 y 33, Apto 39,**

**Playa  
La Habana(CU)**  
Inventor: **González Blanco, Sonia  
Calle 184 No.3112, entre 31 y 33, Apto 42,  
Playa  
La Habana(CU)**  
Inventor: **Santos, Beatriz Tamargo  
Calle 202 No.29302, entre 293y295, Reparto  
Calixto  
Sánchez, Boyeros, La Habana(CU)**  
Inventor: **del Valle Rosales, Jes s Augusto  
D'Strampes N.351, entre San Mariano y Vista  
Alegre  
La Vibora, La Habana(CU)**  
Inventor: **Menéndez, Evelin Caballero  
Calle 7 No.214, entre 2 y 4, Cayo de la Rosa  
Bauta, La Habana(CU)**  
Inventor: **Alvarez Acosta, Anabel  
Calle 184 No.3112, entre 31 y 33, Apto 1,  
Playa  
La Habana(CU)**  
Inventor: **Couzeau Rodriguez, Edelgis  
Calle 184 No.3112, entre 31 y 33, Apto 20,  
Playa  
La Habana(CU)**  
Inventor: **Cruz Le n, Silian  
Ave 47 No.11812, entre 118 y 120, Marianao  
La Habana(CU)**  
Inventor: **Musacchio Lasa, Alexis  
Calle 128 No.7117, entre 71 y 73, Mariel  
La Habana(CU)**

(74) Representative: **Smulders, Theodorus A.H.J.,  
Ir. et al  
Vereenigde Octroobureaux, Nieuwe  
Parklaan 97  
NL-2587 BN Den Haag(NL)**

(54) **Nucleotide sequence coding for an outer membrane protein from Neisseria meningitidis and use**

of said protein in vaccine preparations.

- (57) The present invention is concerned with a method for the isolation of a nucleotide sequence which codes for a protein having a molecular weight of about 64 000 daltons, which is located on the outer membrane of *N. meningitidis*, as well as with the recombinant DNA obtained therefrom, which is used for the transformation of a host microorganism. The technical object pursued with the invention is the identification of a nucleotide sequence coding for a highly conserved and common protein for the majority of pathogenic *Neisseria* strains, the production of this protein with a high level of purity and in commercially useful amounts using the recombinant way, so that it can be used in diagnostic methods and vaccine preparations with a broad immunoprotection spectrum.

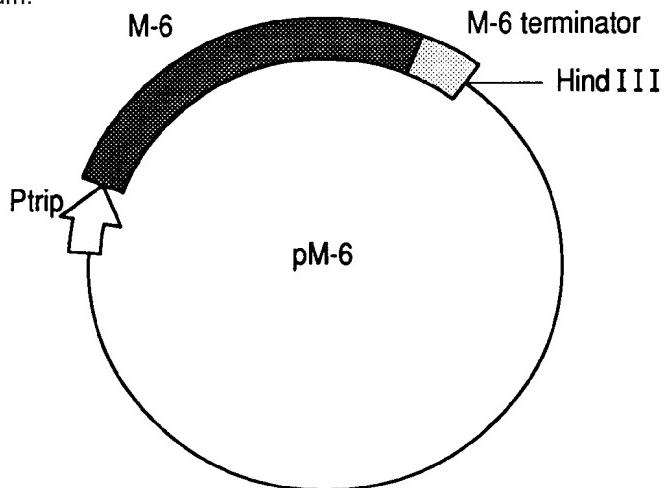


FIG. 1

The present invention is in the field of Genetic Engineering and Biotechnology. More in particular, the invention is related to a nucleotide sequence obtained from the pathogenic bacterium *Neisseria meningitidis*, which nucleotide sequence codes for a protein belonging to the outer membrane of said bacterium. Said protein is cloned and expressed in the host *Escherichia coli*. The characteristics of this protein as well as its capacity to induce immunologically active antibodies (bactericidal antibodies) in its natural host, allow its use in vaccine preparations against pathogenic strains of this microorganism.

The gram-negative bacterium *N. meningitidis* is responsible for one of every three cases of bacterial meningitis in the world. It was described for the first time by Anton Weichselbaum in 1887 (I. DeVoe, 1982, *Microbiol. Revs.* 46: 162-190), and man (i.e. human beings) is its only natural host up to date.

In the first half of this century some essential aspects were found in relation to the metabolism and serological differentiation of this microorganism. The first unsuccessful attempts to obtain vaccine preparations were based on its capsular polysaccharide (E. Kabat et al., 1945, *J. Exp. Med.* 80: 299-307). According to the chemical composition of this capsular polysaccharide, the bacterium *N. meningitidis* is serogrouped in A, B, C, 29-E, H, I, K, L, W-135, X, Y or Z, and the major percentage of illness is caused by A, C, Y, W-135 and B. Non-encapsulated strains are not associated with the invasive disease.

Using different methods of purification of these polysaccharides (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) the four first polysaccharides (PS) showed to be good immunogens and inducers of bactericidal antibodies in humans (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1367-1384). The presence of this kind of antibodies has been correlated previously with non-susceptibility to the infection (I. Goldschneider et al., 1969, *J. Exp. Med.* 129: 1307-1326). As of today mono-, bi- or tetravalent vaccines have been well studied for serotypes A, C and W-135 (F. Ambrosch et al., 1983, *Bulletin of the WHO* 61: 317-323; I. Vodopija et al., 1983, *Infect. Immunol.* 42: 599-604; M. Cadoz et al., 1985, *Vaccine* 3: 340-342; H. Peltola et al., 1985, *Pediatrics* 76: 91-96).

These vaccines have been licensed for their use in humans in different countries (Centers for Disease Control, 1985, *Morbid. Mortal. Weekly Report* 34: 255-259) and some of them are commercially available from different firms and producers (Connaught Laboratories, USA; Smith Kline-RIT, Belgium; Institute Merieux, France; Behringwerke Aktiengesellschaft, Germany; Istituto Sieroterapico e Vaccino genea Toscano "Sclavo", Italy; Swiss Serum and Vaccine Institute, Berne, Switzerland; among others).

However, the conventional vaccine against *N. meningitidis* serogroup C does not induce sufficient levels of bactericidal antibodies in children under 2 years old, which are the principal victims of this disease. It has been demonstrated that the titer of specific antibodies against *N. meningitidis* in children under four years of age, after three years of vaccination, is similar in vaccinated and in non-vaccinated ones (H. Kayhty et al., 1980, *J. of Infect. Dis.* 142: 861-868). Also, no memory response was found against *N. meningitidis* after 8 years of vaccination in young adults (N. Rautonen et al., 1986, *J. of Immunol.* 137: 2670-2675).

The polysaccharide corresponding to *N. meningitidis* serogroup B is poorly immunogenic (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) and induces a poor response of IgM of low specificity (W. Zollinger et al., 1979, *J. Clin. Invest.* 63: 836-848). There are different theories related to this problem, such as cross-reactivity between B polysaccharide and fetal brain structures, antigenic structures modified in solution and sensitivity to neuroaminidases (C. Moreno et al., 1985, *Infect. Immun.* 47: 527-533). Recently, a chemical modification of PS B was achieved, which induced a response in the host (H. Jennings et al., 1988, US Patent 4 727 136; F. Ashton et al., 1989, *Microb. Pathogen.* 6: 455-458), but safety of this vaccine in humans has not been demonstrated.

Due to the lack of an effective vaccine against *N. meningitidis* B, and because the risk of endemic infection is low and mainly restricted to children, a routine immunization with polysaccharides is not recommended (C. Frasch, 1989, *Clin. Microbiol. Revs.* 2: S134-S138) except in the case of an epidemic.

Since after the Second World War the disease was caused in most of the cases by *N. meningitidis* B, vaccines against serogroup B gained special significance.

Other outer membrane components of *N. meningitidis* include phospholipids, lipopolysaccharides (LPS or endotoxins), pili proteins and others. Different immunotypes of LPS have been described for *N. meningitidis* (W. Zollinger and R. Mandrell, 1977, *Infect. Immun.* 18: 424-433; C.M. Tsai et al., 1983, *J. Bacteriol.* 155: 498-504) and immunogenicity using non-toxic derivatives was assayed (H. Jennings et al., 1984, *Infect. Immun.* 43: 407-412) but their variability (H. Schneider et al., 1984, *Infect. Immun.* 45: 544-549) and pyrogenicity (when it is conjugated to lipid A) are limiting factors up to now.

The pili, structures needed to fix cells to nasopharyngeal mucous membrane (D. Stephens et al., 1983, *The J. Infect. Dis.* 148: 369-376) have antigenic diversity among different strains (J. Greenblatt et al., 1988, *Infect. Immun.* 56: 2356-2362) with some common epitopes (D. Stephens et al., 1988, *The J. Infect. Dis.* 158: 332-342). Presently there are some doubts in relation to the effectiveness of a vaccine based on these structures. However some of these types of vaccine have been obtained, without known results related to

their use in humans (C. Brinton, 1988, US Patent 4 769 240).

Recently, the attention has switched to the other proteins of the outer membrane of this bacterium. There are many immunological types of these protein complexes.

The strains of *N. meningitidis* are subdivided in serotypes according to the presence of specific epitopes in the majoritary protein P1/P2 and in subtypes according to other epitopes in protein P1 (C. Frasch et al., 1985, Rev. Infect. Dis. 7: 504-510).

There are several published articles and patent applications concerning vaccines based on cocktails of these proteins, with previous selective removal of endotoxins using biocompatible detergents. The immunogenicity of these cocktails in animals and humans has been demonstrated (W. Zollinger et al., 1979, J.

Clin. Invest. 63: 836-848; C. Frasch and M. Peppler, 1982, Infect. Immun. 37: 271-280; E. Beuvery et al., 1983, Infect. Immun. 40: 369-380; E. Rosenqvist et al., 1983, NIPH Annals 6: 139-149; L. Wang and C. Frasch, 1984, Infect. Immun. 46: 408-414; C. Moreno et al., 1985, Infect. Immun. 47: 527-533; E. Wedege and L.

Froholm, 1986, Infect. Immun. 51: 571-578; C. Frasch et al., 1988, The J. Infect. Dis. 158: 710-718; M.

Lifely. and Z. Wang, 1988, Infect. Immun. 56: 3221-3227; J. Poolman et al., 1988, In J. Poolman et al (Eds), Gonococci and Meningococci, Kluwer Academic Publishers, Dordrecht, The Netherlands, pp 159-165; E. Rosenqvist et al., 1988, J. Clin. Microbiol. 26: 1543-1548), including results in massive field trials e.g. Capetown, South Africa in 1981 (C. Frasch, 1985, Eur. J. Clin. Microbiol. 4: 533-536); Iquique, Chile, 1987 (W. Zollinger, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway

Gardens Conference Center) and Cuba 1986 and 1988 (G. Sierra, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center). However, with the exception of the last case, the bactericidal antibodies induced by these preparations were restricted to the same serotype strains or related ones.

One of these vaccines is referred to in US patent 4,601,903 which is restricted to one of the *Neisseria*

types producing meningitis (serotype 2), with a high incidence, but also other serotypes have been isolated with high frequency from patients, such as serotypes 4 (Cuba from 1981 to 1983, H. Abdillahi et al., 1988, Eur. J. Clin. Microbiol. Infect. Dis. 7: 293-296; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scand. J. Infect. Dis. 21: 527-535); 8 (Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291) and 15 (Norway from 1982 to 1984, L. Froholm et al., 1985, Proceedings of the Fourth International Symposium on Pathogenic Neisseria. American Society for Microbiology; Chile from 1985 to 1987, S. Ruiz et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center) as well as strains of undefined serotype (F. Ashton et al., 1980, Can. J. Microbiol. 26: 1480-1488; Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scan. J. Infect. Dis. 21: 527-535).

The Cuban vaccine achieved in 1988 by the Centro Nacional de Biopreparados (European Patent Application. No. 301 992) has proven to be very effective. It is based on a high molecular weight antigenic complex. It possesses a broad range of cross-reactivity with other strains and produces and maintains bactericidal antibodies in the immunized host.

However, the methods employed to obtain this type of vaccine start with the multiplication in an

appropriate culture of a microorganism which is highly pathogenic, with the associated biological risk of handling directly the bacteria. Moreover, this kind of preparation contains lipopolysaccharides, a contaminant that, although it may increase the product's effectiveness, shows at the same time undesirable secondary effects because of its powerful pyrogenicity. Also, its variation in minor antigenic components, which form part of the preparation, cannot be controlled in the different batches, which makes it difficult to follow important parameters related to the reactogenicity and immunogenicity.

For this reason, there is increasing interest in the identification of nucleotide sequences coding for highly conserved proteins in all strains, and even more so the identification of inducer proteins of bactericidal antibodies common to the majority of pathogenic *Neisseria*, in order to obtain vaccine preparations with a broad spectrum of protection.

There are different proteins with high molecular weight which are present in low amounts in the outer membrane of *N. meningitidis* when this microorganism is grown in conventional culture media but have a strong response in affected individuals (J. Black et al., 1986, Infect. Immun. 54: 710-713; L. Aoun et al., 1988, Ann. Inst. Pasteur/ Microbiol. 139: 203-212) and/or increase their response under special culture conditions (J. van Putten et al., 1987, Antoine van Leeuwenhoek 53: 557-5564; A. Schryvers and L. Morris,

1988, Molecular Microbiol. 2: 281-288 and Infect. Immun. 56: 1144-1149). Some of these proteins are highly conserved among the different strains, in particular those related to the acquisition of iron by the microorganism, that have become interesting vaccine candidates (L. Mocca et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center; C. Frasch,

1989, Clin. Microbiol. Revs. 2: S134-S138).

In addition to pure proteins obtained from the micro-organism or strains of related species (e.g. 37 kD protein, T. Mietzner and S. Morse, 1987, US Patent 4 681 761), several related genes have been cloned and expressed. Among these proteins are the following:

- 5 protease IgA1 (J. Koomey and S. Falkow, 1984, Infect. Immun. 43: 101-107);
- protein P1 (A. Barlow et al., 1987, Infect. Immun. 55: 2734-2740, and 1989, Molec. Microbiol. 3: 131-139);
- protein P5a (T. Kawula et al., 1988, Infect. Immun. 56: 380-386);
- protein P5c (T. Olyhoek and M. Achtman, 1988, Proceedings of the Sixth International Pathogenic N. Conference. Callaway Gardens Conference Center);
- 10 protein P4 (K. Klugman et al., 1989, Infect. Immun. 57: 2066-2071);
- protein P2 (K. Murakami et al., 1989, Infect. Immun. 57: 2318-2323);
- and from *N. gonorrhoeae*, which code for proteins with cross-reactivity with their corresponding proteins from *N. meningitidis*:
- antigen H.8 (W. Black and J.G. Cannon, 1985, Infect. Immun. 47: 322-325);
- 15 macromolecular complex (W. Tsai and C. Wilde, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center);
- 37 kDa protein, repressed in the presence of iron (S. Berish et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center).

The use of these proteins as active vaccine preparation has not been reported or the bactericidal tests of antibodies induced against them were negative, such as in the case of mouse monoclonal antibodies against H.8 (J. Woods et al., 1987, Infect. Immun. 55: 1927-1928).

Up to the moment, the protein P1 located in the outer membrane of *N. meningitidis* is one of the best characterized and studied antigens. This protein presents no variability within the same strain. However, there are more than 17 types of proteins P1 in *Neisseria* which have differences in three variable regions, 25 this being the basis of the classification of *N.* in different subtypes. This protein is very immunogenic in humans (W.D. Zollinger and R.E. Mandrell, 1983, Med. Trop. 43:143-147), eliciting protective antibodies (E. Wedege and L.O. Froholm, 1986, Infect. Immun. 51: 571-578; K. Saukkonen et al, 1987, Microb. Pathogen. 3:261-267), that give it a special importance in vaccine preparations.

Some subtypes of proteins P1 have been cloned in *E. coli*, starting from genomic libraries (A.K. Barlow et al., 1989, Molec. Microb. 3:131-139) or using the PCR technique (S. Butcher et al., VIIth International Congress of *Neisseria*, R.C. Seid, Patent Application WO 90/06696; Brian Mc Guinness et al., 1990, J. Exp. Med. 171:1871-1882, M.C.J. Maiden et al., VIIth International Conference of *Neisseria*, Berlin, Sept. 9-14, 1990, and 1991, Molec. Microb. 3:727; J. Suker et al., VIIth International Conference of *Neisseria*, Berlin, Sept. 9-14, 1990). However, up to now, there is no genetic construction able to produce this protein with 35 high levels of expression. Only low levels of expression (D.A. White et al., 1990, Molec. Microb. 4:769:776) or its expression in *Bacillus subtilis* fused to the outer membrane protein A of *E. coli* (omp A) (E. Wahlstrom et al., VIIth International Congress of *Neisseria*, September 9-14, 1990, Berlin) have been reported.

It can be affirmed that up to the moment no antigen has been isolated which is common to all types and serogroups of *N. meningitidis* and is able to produce bactericidal antibodies. For this reason, an antigen 40 of this kind, conjugated or fused to other proteins or polysaccharides of immunological interest, would be relevant as a candidate for bivalent vaccine preparations.

This invention is related to a nucleotide sequence coding for a protein having a molecular weight of about 64 kilodaltons. This sequence has been found in all *N. meningitidis* serotypes and serogroups tested, as verified by nucleic acid hybridization, Western-blotting, Dot-blot and ELISA.

45 A technical object of this invention is the identification of a nucleotide sequence which codes for a highly conserved protein and is common to the majority of pathogenic strains of *Neisseria* (named P64k), in order to obtain the protein by a recombinant way with a high grade of purity and in commercially useful quantities, so that it can be employed in diagnostic methods and as an integrating part of a vaccine preparation of broad spectrum of protection.

50 On the level of genetic information (DNA and RNA), the invention provides a recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of *Neisseria meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. In a preferred embodiment said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1. The recombinant polynucleotide may further comprise a 55 nucleotide sequence of a cloning or expression vector.

The invention also provides a transformed microorganism containing a recombinant polynucleotide as defined above, preferably a transformed microorganism which is capable of expressing the protein P64k of *N. meningitidis*. In a particularly preferred embodiment of the invention, the transformed microorganism is

an Escherichia coli strain, e.g. E. coli strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of N. meningitidis, e.g. the expression vector pM-6.

The invention also provides a recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of N. meningitidis,

5 said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. Said recombinant proteinaceous substance may essentially consist of protein P64k, or be a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of N. meningitidis.

The invention further provides a vaccine composition, comprising a recombinant protein as defined above, together with a suitable carrier, diluent or adjuvant. A particular embodiment of this invention 10 provides a vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of N. meningitidis, together with a suitable carrier, diluent or adjuvant.

In addition, the invention provides a monoclonal antibody, raised against a recombinant proteinaceous substance as defined above, or against a lipoamide dehydrogenase or acetyl transferase, and capable of 15 binding a protein P64k of N. meningitidis.

The invention also provides a process for preparing a protein P64k of Neisseria meningitidis, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed 20 microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.

One novel aspect of this invention is the gene isolated from the N. meningitidis strain B:4:P1.15, which was named M-6 and has as a principal characteristic its stability in E. coli vectors. This gene does not produce adverse effects on the host, allowing to obtain yields of over 25 % of total protein (ratio of P64k to 25 total protein from host strain). On the other hand, it has been demonstrated by Southern and Western Blot hybridizations (E. Southern, 1975, J. Mol. Biol. 98: 503-527 and W. Burnette, 1981, Anal. Biochem. 12: 195-203) that protein P64k is present in all the following studied strains of N. meningitidis:

N. meningitidis A

N. meningitidis B:1

30 N. meningitidis B:2

N. meningitidis B:4

N. meningitidis B:5

N. meningitidis B:8

N. meningitidis B:9

35 N. meningitidis B:11

N. meningitidis B:15

N. meningitidis B:4:P1.15

N. meningitidis C

N. meningitidis B:15:P1.16

40 N. meningitidis B:15:P1.16 (H 44/76)

N. meningitidis B:NT (121/85)

N. meningitidis B:NT (71/86)

N. meningitidis B:NT (210/86)

and also in N. mucosa, N. subflava and N. gonorrhoeae.

45 The protein is not present in N. cinerea, N. lactamica, N. sicca and N. flavescens, but these are not of interest because they are not pathogenic.

The protein having a molecular weight of about 64 kDa can be localized by electron microscopy in the outer membrane of N. meningitidis. Therefore, this antigen is an exposed antigen which is favorable for use in a vaccine preparation. The protein was recognized in Western blot immunoidentification experiments with 50 sera from convalescents and individuals vaccinated with the conventional Cuban vaccine Va-Mengoc-BC (Centro Nacional de Biopreparados, Havana, Cuba). This aspect guarantees the immunogenicity of the antigen and at the same time confirms its presence within the high molecular weight protein fraction constituent of this vaccine, which is responsible of the lasting immune response to the disease.

Another novel aspect is that the protein, which is an object of this invention, produces antibodies with a 55 broad bactericidal spectrum (different serogroupes, serotypes and subtypes), a characteristic which has not been reported previously for any protein from N. meningitidis.

This protein obtained in high levels in E. coli becomes an important candidate for the improvement of immunogenicity when expressed as a fusion protein with other proteins. It could also increase the

expression by conferring enhanced stability and suitability in the molecular structure during transcription and translation processes. Belonging to *Neisseria*, this protein can also be fused to other proteins from *Neisseria* in order to obtain vaccine preparations against this microorganism with increased immunogenicity. These fusion proteins are also objects of this invention.

5 On the other hand, surprisingly, it was found that the gene M-6 obtained from a genomic library of the strain *N. meningitidis* B:4:P1.15 showed a great homology with sequences of lipoamide-dehydrogenases and acetyl-transferases from other microorganisms and higher organisms. The presence of common antigenic determinants allows the use of these other related proteins as immunogens, able to confer protection by the induction of bactericidal antibodies which recognize the antigenic determinants common 10 to protein P64k. Therefore, the use of these lipoamide-dehydrogenases and acetyl-transferases (not isolated from *N. meningitidis*) or derivatives therefrom such as peptides, fragments from enzymatic degradation, constructions of fusion with other proteins, or conjugation with proteins, polysaccharides or lipids, or insertion in complexes as liposomes or vesicles, etc., for vaccine purposes, are included in the scope of this invention.

15 An important object of this invention is the nucleotide sequence which codes for the M-6 gene (SEQ ID NO:1 of the Sequence Listing) whose product is the protein P64k.

This gene was derived from the genome of the strain B385 isolated in Cuba (*N. meningitidis* B:4:P1.15), by the construction of a genomic library in the phage EMBL 3.

20 The recombinant DNA including the gene M-6 constitutes another object of this invention, which includes the phage lambda, the plasmid pM-3 and the expression vector pM-6 for expression in bacteria.

In particular, for the intracellular expression in *E. coli*, the M-6 gene was cloned under the tryptophane promotor and using its own termination signal of transcription and a linkage fragment between M-6 and the cloning site Ncol which adds the following nucleotide sequence at the 5' end:

ATG CTA GAT AAA AGA (SEQ ID NO:2)

25 The N-terminal of the protein P64k encoded by the M-6 gene inserted in plasmid pM-6 which adds 5 aminoacids to the N-terminal of the original protein corresponds to:

M L D K R M A L V E L K V P D I G G H E N V D I I (SEQ ID NO:3)

Another object of this invention are the microorganisms resulting from the transformation of *E. coli* strain HB 101 with the pM-6 vector, which are characterized by the expression of high levels of protein P64k, good 30 viability and great stability.

The transformed clone of *E. coli* was denominated HBM64 (Fig. 2), and presents levels of expression of P64k higher than 25 % in relation to the total protein of the cell (Fig. 6).

The procedure described in the present invention, due to the levels of expression achieved for this product, allows to reach an optimal purity for use of this protein in humans.

35 On the other hand, the antigen obtained from the isolated sequence was very useful in the preparation of different types of potential vaccine preparations, like bivalent vaccines with a broad immunoprotective spectrum, e.g., protein-polysaccharide conjugates, fusion proteins, etc.

**EXAMPLES:** These examples intend to illustrate the invention, but not to limit the scope of this invention.

40

#### EXAMPLE 1:

For the isolation of genomic DNA from *N. meningitidis* B:4:P1.15, the cells were grown in Mueller-Hinton medium (OXOID, London). The biomass from a culture of 100 ml was resuspended in 8 ml of Tris 45 (hydroxymethyl-aminomethane) 100 mM, EDTA (ethylenediamine tetraacetic acid) 1mM, pH 8. The cells were subjected to a treatment with lysozyme (10 mg/ml), followed by 200 µl of self-digested pronase (20 mg/ml) and 1.1 ml of 10% SDS. The mixture was incubated at 37 °C during 1 hour, then it was treated with phenolchloroform (v/v) and the remains of phenol were eliminated using 2-butanol. Finally, the DNA was precipitated with absolute ethanol and RNA was eliminated with ribonuclease A (Sigma, London).

50 The DNA of about 60 kb was subjected to a partial digestion with the enzyme Sau 3A, obtaining a population of fragments of about 15 kb. This majoritary fraction was isolated and purified by separation in agarose gel (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY).

55 For the construction of the genomic library, the process described by Maniatis was essentially followed (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY). Four µg of purified DNA were ligated with 8 µg of BamHI-digested EMBL-3. The ligation product was packed and the phages were finally plated on the *E. coli* strain C66P2.

The library was screened by immunoidentification (R. Young and R. Davis, 1983, PNAS USA 80: 1194-

1198) using rabbit serum obtained against a preparation of proteins belonging to the outer membrane of the strain *N. meningitidis* B:4:P1.15. The clones were analyzed by Western blot (Burnette, 1981) and the expression of the P64k protein with a molecular weight of about 70 kDa was detected. The resulting recombinant phage was named 31. The Western blot was also made using a mixture of sera from 5 convalescents of meningococcemia, free of antibodies from *E. coli*, obtaining the same result as that using hyperimmunized rabbit sera.

This experiment was repeated using sera from several healthy individuals, and the signal obtained was negative against the recombinant protein P64k.

10 EXAMPLE 2:

For subcloning in bacteria, the 17 kb insert corresponding to the phage isolated from the library was cloned in the plasmid pUC18 after separation from the phage's arms using the enzyme Sall. This resulted in the construction pM-1 (Fig. 2), that was subjected to restriction analysis (Fig. 3).

15 The fragment Sall-HindIII of about 6 kb was recloned in the plasmid pUC18 and the construction pM-2 was obtained (Fig. 2). In order to obtain a more exact localization of the gene coding for protein P64k deletions were carried out with the enzymes Clal, EcoRI and Hincll. The complete fragment of the gene M-6 was finally localized as an EcoRI-HindIII insert corresponding to the construction pM-3 (Fig. 2).

In all constructions, the presence of the gene was confirmed by recognizing the protein by colony 20 immunoidentification and Western Blot using hyperimmunized rabbit sera.

The sequence of the insert in pM-3 was determined by the method of Sanger (F. Sanger et al., 1977, PNAS USA 74: 5463-5467).

From the obtained sequence, the approximate molecular weight of the protein encoded by the gene was deduced.

25 In order to obtain a construction for high expression of the protein P64k, the plasmid pM-3 (Fig. 2) was linearized with the enzyme EcoRI and successive suppressions of the gene were carried out, incubating the sample with the nucleases ExoIII and S1.

The resulting fragments were separated from the rest of the vector pUC18 by cutting with the restriction enzyme HindIII and were cloned fused to a stabilizer fragment (European patent application EP-A-0 416 30 673), using an Xba-blunt adapter to conserve the XbaI site of the stabilizer gene:

5' C T A G A T A A A A G A 3' (SEQ ID NO:4)

35 3' T A T T T T C T 5' (SEQ ID NO:5)

The constructions in which the fused fragment coincided with the reading frame were selected by 40 immunoidentification using hyperimmune rabbit sera.

The insert sequences were established using Sanger's Method (F. Sanger et al., 1977, PNAS USA 74: 5463-5467). From the obtained sequences the approximate molecular weight of the protein encoded by this gene was deduced.

The fusion region between the proteins was localized in the gene sequences. In the clone pILM-25 45 (Figure 4) the ATG of the gene predetermined by the sequence of the DNA insert isolated from the library, coincided with the fusion site.

The Ncol-XbaI fragment, corresponding to the stabilizing peptide coding sequence, was deleted from pILM-25, obtaining a non-fused protein expressed under the tryptophan promoter with its original terminator from the *N. meningitidis* B:4:P1.15, according to the pM-6 construction (Figure 1).

50 The pM-6 plasmid was transformed in different strains of *E. coli* like W3110, JA-221, HB-101, LE-392 and MC-1061, and the expression of P64k was compared. The best results were obtained in W3110, JA-221 and HB-101. These strains were chosen to scale up fermentation, and expression levels up to 25 % of total cell proteins were obtained.

55 EXAMPLE 3:

To confirm the correct expression of the cloned gene the N-terminal region of the intact protein was subjected to the Edman degradation method (P. Edman, 1950, Acta Chem. Scand. 4: 283-293). This

technique elucidates the sequence (primary structure) of this region in the molecule.

The P64k protein was desalted by gel filtration chromatography (PD-10, Pharmacia), eluted with water and monitored at 280 nm. The protein fraction was concentrated to 0.5 nM/μl. One μl of this solution was applied to a PVDF (polyvinylidene difluoride, Millipore) filter, previously activated with methanol.

5 The Edman degradation was made using the Knauer's Automatic Sequencer, model 810, connected to a HPLC (High Performance Liquid Chromatography) system, so as to detect the phenylthiohydantoin derivatives of the aminoacids (PTH-aminoacids). The standard procedure of sequencing as recommended by the manufacturer of the equipment was followed. The separation of the PTH-aminoacids was performed in a reverse phase column C-18 (5 μm), 250 mm x 2 mm (Merck), eluted with an acetonitrile gradient (B buffer) in sodium acetate (A buffer), prepared according to the manufacturers, with a 200 μl/minute flow and at 42 °C. The PTH-aminoacids were detected at 269 nm.

10 Data processing and registration were made in a Shimadzu model CR-6a automatic integrator, using a program for data processing by subtraction of two consecutive chromatograms, to facilitate the evaluation of the Edman degradation cycles. Sequence identification is obtained by the chromatographic evaluation of the 15 corresponding analyzed cycle and confirmed by the chromatogram obtained by subtraction, allowing to determine 25 residues.

#### EXAMPLE 4:

20 To demonstrate that the protein P64k is recognized by the sera of individuals vaccinated with the Cuban Va-Mengoc-BC preparation (Centro Nacional de Biopreparados, Havana, Cuba.), a Western-Blot was made, with a mixture of 12 sera from adults (immunized with two doses of the Cuban vaccine) diluted in a solution containing defatted milk (Oxoid, London). The experiment included:  
recombinant protein P64k, purified from *E. coli* HB-101 transformed with the pM-6 plasmid;  
25 supernatant of the ultrasonic cell rupture of untransformed *E. coli* HB-101;  
the reaction was revealed with a protein A-colloidal gold conjugate.  
It was shown that the protein P64k is recognized by the pool of sera.

#### EXAMPLE 5:

30 The bactericidal test against B385 (B:4:P1.15) was made according to the procedure described by Lerrick et al. (Scand. J. Immunol. 32, 1990, 121-128) with modifications. With this objective, a mixture was made of a) a suspension of bacteria, cultured under special conditions (1-5 colony forming units/1), b) Gey's balanced salt solution, c) rabbit sera (3 to 4 weeks) as a source of complement and d) pooled sera from 35 mice, immunized against protein P64k in Aluminium Hydroxyde Gel, and inactivated at 56 °C for 30 minutes. The immunization of mice was carried out according to an immunization scheme of 3 doses of 20 μg each. The proportions used in the aforementioned mixture were 1:2:1:1 in a total volume of 125 μl. The mixture was incubated at 37 °C during 1 hour and plated in fresh Mueller Hinton Agar (Oxoid, London) supplemented with 5 % calf serum (CubaVet, Habana). The counting of surviving colonies was done after 40 18 hours of incubation of the plates in an atmosphere of 5 % CO<sub>2</sub> at 37 °C.

The bactericidal titer was considered as the maximum serum dilution necessary to render a 50 % inhibition of bacterial growth, with respect to the same mixture without the test serum. It was found that 1:20 serum dilution still maintains its bactericidal activity. As negative controls (non bactericidal at 1:2 dilution) pooled sera from mice immunized with Aluminum Hydroxyde Gel, and pooled sera from mice immunized 45 with cuban Hepatitis B recombinant vaccine, were used. The bactericidal effect was specific to the anti-P64k antibodies.

#### EXAMPLE 6:

50 The bactericidal test against different strains of *N. meningitidis* was made using:  
1. An ammonium sulphate precipitate of the supernatant harvested from a culture of hybridoma cells secreting monoclonal antibodies specific against P64k (anti P64k)/Sample to analyze.  
2. An ammonium sulphate precipitate of the supernatant harvested from hybridoma cells secreting 55 monoclonal antibodies specific against the P1.15 protein present in *N. meningitidis* strain B385 (anti P1.15)/Positive control of the system.

The maximum dilutions tested were always 1:16. The maximum dilutions tested which had a bactericidal effect, according to the EXAMPLE 5, are indicated:

Strain	anti-P64k	anti-P1.15
B385	1:16	1:16
B:4:P1.15	1:16	1:16
B:14:P1.7	1:16	-
B:NT:NT	1:16	-
B:15:P1.15	1:8	-
B:15:P1.16	1:8	-
B:13	1:8	-
C	1:16	-
A	1:16	-

As seen, the anti-P64k monoclonal antibodies have significant bactericidal titers against different serogroups (A, B and C), serotypes (4, 14, 13, 15 and NT) and subtypes (7, 15, 16 and NT) of bacteria.

## EXAMPLE 7:

Fusion protein M-14 (P64k and P1.15)

In order to obtain a genetic construction for high expression that contained the variable epitopes of the P1.15 protein (Outer membrane protein from *N. meninigitidis* B:4:P1.15) fused to the P64k protein, the gene coding for P1.15 protein was cloned using the Polymerase Chain Reaction (PCR). The following region containing the variable immunodeterminants of P1.15:

```

L Q L T E P P S K S Q P Q V K V T K A K S R I R T K I S D F G
S F I G F K G S E D L G E G L K A V W Q L E Q D V S V A G G G
A T Q W G N R E S F V G L A G E F G T L R A G R V A N Q F D D
A S Q A I D P W D S N N D V A S Q L G I F K R H D D M P V S V
R Y D S P D F S G F S G S V Q F V P I Q N S K S A Y T P A Y H
Y T R Q N N A D V F V P A V V G K P G S D V Y V A G L N Y K N
G G F A G S Y A F K Y A R H A N V G R N A F E L F L L G S T S
D E A
(SEQ ID NO:6)

```

was inserted in the Mlu I site of the gene M-6, encoding for P64k, after having been made blunt with the klenow fragment from DNA polymerase I. The sites for gene fusion of P1.15 with M-6 are the following:

GDALQL

(SEQ ID NO:7)

Gly Asp Ala	Leu Gln Leu	
5' - GGC GAC GCG	CTG CAG TTGA	-3' (SEQ ID NO:8)
M-6	P1.15	

EANAYE

(SEQ ID NO:9)

5

Glu Ala Asn\*Ala Tyr Glu  
 5' - GAA GCC AAC GCG TAC GAA -3' (SEQ ID NO:10)  
 P1.15 M-6

10

\*: N does not belong to any of the fusion proteins and was created by the genetic construction.

15

The resulting fusion protein (M-14) was expressed in E. coli using a plasmid vector under the tryptophan promoter, to levels higher than 10 % of total cell protein. The protein was recognized by bactericidal monoclonal antibodies, and anti-P1.15 and P64k polyclonal antibodies, in Western-Blot.

## 20 EXAMPLE 8:

Polysaccharide/P64k conjugation.

The protein P64k was conjugated with the polysaccharide from Haemophilus influenzae using the reductive amination method. The Haemophilus influenzae polysaccharide (Polyribosyl ribitol phosphate, PRP) was purified by the cold phenol method described by Frasch, 1990 (in: Bacterial Vaccines, 1990, Alan R. Liss, Inc., pp. 123-145). The final contamination of PRP with proteins or nucleic acids was less than 1 %. This polysaccharide was degraded using the method of Parikh et al. 1974 (Methods in Enzymol. 34B: 77-102) with sodium periodate in PRP (ratio 1 : 5 w/w) dissolved in 0.1 M sodium acetate (pH 4.5). The incubation was carried out in the dark during 30 minutes with stirring. The periodate excess was eliminated by addition of ribitol. Very low molecular weight compounds were eliminated by dialysis (Medicell International Ltd. Membrane, London). The resulting oligosaccharide had free aldehyde groups able to react with primary amines (e.g. lysine residues in proteins). The conjugate is obtained by mixing protein and polyssacharide in a 1 : 1 ratio (w/w), adding sodium cyanoborohydride and subjecting the mixture to an incubation, first for 48 hours at 4 °C and later at 37 °C for 24 hours. The high molecular weight complex which contains the resulting conjugate with protein-polysaccharide in a 1 : 2.3 ratio, can be separated from the non reactive contaminants by HPLC.

## EXAMPLE 9:

40

Bivalent vaccine preparation against Hepatitis B virus and N. meningitidis.

In order to obtain a bivalent vaccine preparation, different quantities of protein P64k and Hepatitis B Surface Antigen (Vacuna Recombinante contra 1a Hepatitis B, Heber Biotec, Havana, Cuba) were mixed. The antigens were adjuvated with Aluminum Hydroxyde Gel, at 2mg/dose and inoculated in Balb/c mice having a body weight of 20 g in 3 dosis of 0.5 ml each. Different variants were assayed:

1. P64k 20 µg (P20)
2. HBsAg 20 µg (H20)
3. P64k 10 µg + HBsAg 10 µg (P10:H10)
4. P64K 15 µg + HBsAg 5 µg (P15:H5)
5. Placebo (Al(OH)<sub>3</sub>)

50

Seven days after the immunization with the first doses, the second doses were applied. The third dose was given 14 days after the second. Seven days later, blood was taken and the serum of each immunized animal was separated. Antibody titers against P64k protein were measured in solid phase Enzyme Linked Immunosorbent Assay (ELISA), using P64k at 5 mg/ml to coat the polystyrene plate. The antibody titers against HBsAg were determined by a Commercial ELISA (Organon Teknika, Boxtel). Figure 5 shows the dynamics of antibody response against protein P64k, using sera diluted 1/10 000. The response against P64k is not interfered by the presence of the other antigen. Figure 6 shows the titers against HBsAg after each dosis. The titers against this protein are not diminished by the presence of P64k in the preparation.

High titers are obtained against both antigens in the same vaccine preparation.

### EXAMPLE 10:

- 5 A software was created to search the EMBL (European Molecular Biology Laboratory) Data Base and  
detect the homology between P64k and other proteins. As result of the search it was found that there is  
homology of one segment in the sequence of P64k with segments in the sequences of *N. gonorrhoeae*.  
This sequence was found as characteristic in both *N. gonorrhoeae* and *N. meningitidis* (F.F. Correia, S.  
Inouye and M. Inouye, 1988, J. Biol. Chem. 263, No. 25, 12194-12198).  
10 Another region with high homology was found in two proteins of the Pyruvate Dehydrogenase Complex  
from *E.coli* K12:

a) Acetyltransferase from *E. coli* and the P64k outer membrane protein from *N. meningitidis*.

- 15 Homology exists between a segment comprising 100 amino acids, repeated at the beginning of the  
amino acid sequence of the Acetyltransferase ("Lipoyl Domain", including the "Lipoyl Binding Site" (P.E.  
Stephens et al., 1983,. Eur. J. Biochem. 133, 481-489)) and a region located in the first 111 amino acids of  
the P64k:

20 MALVELKVPDIGHENVDIIIAVEVNVGDTIAV (SEQ\_ID\_NO:11)  
- \* - \*\*\*\*\* - \*-- \* \* \*\*\* -\*  
VKEVNVPDIGG DEVEVTEVMVKVGDVKAA (SEQ\_ID\_NO:12)

25 DDTLITLEDKATMDVPAEVAGVVKEVKVKVG (SEQ ID NO:11) (cont)  
-- \*-\*-\* \*-\*-\* \*-\*-\*-\*-\*-\*-\*  
EQSLITVEGDKASMEVPAPFAGVVKELKVNVG (SEQ ID NO:12) (cont)

<sup>30</sup> DKISEGGGLIVVVEAEGT--AAPKAESAA--A (SEQ ID NO:11) (cont)  
\*\*- \* \*\*- \* \* \* \*\*\*\* - \* \* \*  
DKVKTGSLIMIFEVEGAAPAAAPAKOEAAAPA (SEQ ID NO:12) (cont)

35 PRKKPLKCRWVPQAAQFGG (SEQ ID NO:11) (cont)  
\* \* \* \* \*  
PAAKAEAPAAAPAAKAEGK (SEQ ID NO:12) (cont)

40 where (\*) indicates positions with the same amino acids and (-) indicates positions of conservative amino acid changes.

b) Lipopeptide Dodecaspanoyl from *E. coli* and Outer Membrane PC41c protein from *N. meningitidis*

45 Homology exists between the Lipoamide Dehydrogenase from *E. coli* (a protein having 473 amino acids, P.E. Stephens et al., 1983, Eur. J. Biochem. 133, 481-489) and the protein P64k, specifically in a segment which represents almost the total protein, except the region with homology with the "lipoyl domain" from Acetyltransferases.

5                     ---1---   SADA EYDV VV LGGG PG YSAF AA DE GLKVA * --- - * * * * - * * * * * * * * * * * --- STE IKTQ VV VL GAG PAG YSAF RCAD LGLETV	(SEQ ID NO:13)  (SEQ ID NO:14)
10                    -----2-----   I VERY KTL GG VCL NV GCIP SKALL HNA AV IDE * * * * - * * * * * * * * * * * * * * * * * --- I VERY NTL GG VCL NV GCIP SKALL HVAK VIEE	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
15                  VRHL AANG IKY PEP ALD ID MRL RAY KDG VVS RL -- * * -- * - * * * * * * * * * * * * * * --- AKAL AE HGIV FGE PKTD ID KI TW KE KV IN QL	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
20                  TG-FGRY GE KR KV DV VI QGD GQ FLD PH HLE VSL ** -- - - * * * * * * * * * * --- * * --- * * --- TG GLA GM AK GR KV KV VN GL GK FT GANT LE VEG	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
25                  TAG DAY EQA AP TGE KK IV AF KNC II AAG SR VT -- * --- ENG ----- KTV INF DN AII AAG SR PI	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
30                  KL PF IP-ED PR IID SSG GAL AL KE VP GKL LI IG - * --- QL PF IP HED PR IW DSTD AEL KE VP ER LL VM G	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
35                  GGI IGL EM GTV YST LGS RLD VV EMM DGL MQ GA * --- GGI IGL EM GTV YHAL GS QID VV EMD QV IP AA	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
40                  DRD LV KV WQ KQ NE YRF DN IM VNT KTV AVE PKE * - * * * - * - - - * - * - * - * - * * * * --- DKD IV KV FTK RISK KFN - LM LET KVT AVE AKE	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
45                  DG VY VT FEG AN PP KEP QR YDA VL VA AG RA PNG * * - * * * - * * - * * * * * * * * * * * * --- DG IY VT MEG KK KAP AEP QR YDA VL VA IGR VP PNG	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)
50                  KL IS AE KA GV AV TD RG FIE VD KQM RTN VP HI Y * - - * - * * * - * - * * * * * * * * * * --- KN LD AG KAG VE VD DR GF IR VD KQL RTN VP HI F	(SEQ ID NO:13) (cont)  (SEQ ID NO:14) (cont)

AIGDIVGQPMLAHKAVHEGHVAAENCAGTKAY ***** AIGDIVGQPMLAHGVHEGHVAAEVIAGKKHY	(SEQ ID NO:13) (cont) (SEQ ID NO:14) (cont)
5	
FDAAVIPGVAYTSPEVAWVGETELSAKRPGK ***- ***-***-***** * -** - - FDPKVIPSIAYTEPEVAWGLTEKEAKEKGIS	(SEQ ID NO:13) (cont) (SEQ ID NO:14) (cont)
10	
ITKANFPWAASGRAIANGCDKPFTKLIFDAET *-*****-**- - - -***** * - YETATFPWAASGRAIASDCADGMTKLIFDKES	(SEQ ID NO:13) (cont) (SEQ ID NO:14) (cont)
15	
GRIIGGGIVGPNGGDMIAKSALPSKLGCDAAAD *-***-***-***- - - - -***** * - HRVIGGAIVGTLNGGELLGEIGLAIEMGCDAED	(SEQ ID NO:13) (cont) (SEQ ID NO:14) (cont)
20	
--3-   VGKTIHPRPTLGESIGMAAEVALGTCTDLPPQ -- ***-*** * - - - -***** * - * *** - IALTIHAHPTLHESVGLAAEVFEGSITDLPNP	(SEQ ID NO:13) (cont) (SEQ ID NO:14) (cont)
25	
--KKK - MEN1pd ***	(SEQ ID NO:13) (cont)
KAKKK - EC1pd	(SEQ ID NO:14) (cont)
30	

Where:

- |1-|: Adenine binding site (FAD)
- 35 |2-|: Redox active disulphide region
- |3-|: Active site histidine

Strain deposits:

- 40 An E. coli HB-101 clone containing the plasmid pM-3 (a pUC18 plasmid containing the 4.1 kb DNA fragment from *Neisseria meningitidis*, strain B:4:P1.15, cloned between the EcoRI and HindIII restriction sites), was deposited on August 30, 1991, with the Centraalbureau voor Schimmelcultures (CBS), Baarn, The Netherlands, and obtained deposit number CBS 485 .91.

45

50

55

## SEQUENCE LISTING

5

SEQ ID NO:1

SEQUENCE TYPE : Nucleotide with corresponding amino acid

SEQUENCE LENGTH: 1830 bp

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE ORGANISM: N. meningitidis group B

IMMEDIATE EXPERIMENTAL SOURCE: Strain B:4:P1:15 isolated in  
Cuba

FEATURES: From 1 to 1830 bp mature protein

PROPERTIES: Gene coding for P64k protein from outer membrane  
of N. meningitidis

ATG	CTA	GAT	AAA	AGA	ATG	GCT	TTA	GTT	GAA	TTG	AAA	GTG	CCC	42
Met	Leu	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	
1					5					10				
GAC	ATT	GGC	GGA	CAC	GAA	AAT	GTA	GAT	ATT	ATC	GCG	GTT	GAA	84
Asp	Ile	Gly	Gly	His	Glu	Asn	Val	Asp	Ile	Ile	Ala	Val	Glu	
15					20					25				
GTA	AAC	GTG	GGC	GAC	ACT	ATT	GCT	GTG	GAC	GAT	ACC	CTG	ATT	126
Val	Asn	Val	Gly	Asp	Thr	Ile	Ala	Val	Asp	Asp	Thr	Leu	Ile	
30					35					40				
ACT	TTG	GAA	ACC	GAT	AAA	GCG	ACT	ATG	GAC	GTA	CCT	GCT	GAA	168
Thr	Leu	Glu	Thr	Asp	Lys	Ala	Thr	Met	Asp	Val	Pro	Ala	Glu	
40					45					50			55	
GTT	GCA	GGC	GTA	GTC	AAA	GAA	GTT	AAA	GTT	AAA	GTC	GGC	GAC	210
Val	Ala	Gly	Val	Val	Lys	Glu	Val	Lys	Val	Lys	Val	Gly	Asp	
45					60					65			70	
AAA	ATC	TCT	GAA	GGT	GGT	TTG	ATT	GTC	GTC	GTC	GTT	GAA	GCT	252
Lys	Ile	Ser	Glu	Gly	Gly	Leu	Ile	Val	Val	Val	Val	Glu	Ala	Glu
75														
GGC	ACG	GCA	GCC	GCT	CCT	AAA	GCC	GAA	TCG	GCT	GCC	GCC	CCG	294
Gly	Thr	Ala	Ala	Ala	Pro	Lys	Ala	Glu	Ser	Ala	Ala	Ala	Pro	
85					90					95				

55

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CGC	AAG	AAG	CCC	CTA	AAC	GTG	CCG	CTC	CCT	GCT	CCG	CAA	GCC	336	
Arg	Lys	Lys	Pro	Leu	Asn	Val	Pro	Leu	Pro	Ala	Pro	Gln	Ala		
100						105					110				
5	GCG	CAA	TTC	GGC	GGT	TCT	GCC	GAT	GCC	GAG	TAC	GAT	GTG	GTC	378
	Ala	Gln	Phe	Gly	Gly	Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	
	115					120					125				
10	GTA	TTG	GGT	GGC	GGT	CCC	GGC	GGT	TAC	TCC	GCT	GCA	TTT	GCC	420
	Val	Leu	Gly	Gly	Gly	Pro	Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	
	130					135					140				
15	GCT	GCC	GAT	GAA	GGC	TTG	AAA	GTC	GCC	ATC	GTC	GAA	CGT	TAC	462
	Ala	Ala	Asp	Glu	Gly	Leu	Lys	Val	Ala	Ile	Val	Glu	Arg	Tyr	
	145						150								
20	AAA	ACT	TTG	GGC	GGC	GTT	TGC	CTG	AAC	GTC	GGC	TGT	ATC	CCT	504
	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	
	155					160				165					
	TCC	AAA	GCC	TTG	TTG	CAC	AAT	GCC	GCC	GTT	ATC	GAC	GAA	GTG	546
	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala	Val	Ile	Asp	Glu	Val	
	170					175				180					
25	CGC	CAC	TTG	GCT	GCC	AAC	GGT	ATC	AAA	TAC	CCC	GAG	CCG	GAA	588
	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr	Pro	Glu	Pro	Glu	
	185					190				195					
30	CTC	GAC	ATC	GAT	ATG	CTT	CGC	GCC	TAC	AAA	GAC	GGC	GTA	GTT	630
	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp	Gly	Val	Val	
	200					205				210					
35	TCC	CGC	CTC	ACG	GGC	GGT	TTG	GCA	GGT	ATG	GCG	AAA	AGC	CGT	672
	Ser	Arg	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Ser	Arg	
	215						220								
40	AAA	GTG	GAC	GTT	ATC	CAA	GGC	GAC	GGG	CAA	TTC	TTA	GAT	CCG	714
	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro	
	225					230				235					
	CAC	CAC	TTG	GAA	GTG	TCG	CTG	ACT	GCC	GGC	GAC	GCG	TAC	GAA	756
	His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	
	240					245				250					
45	CAG	GCA	GCC	CCT	ACC	GGC	GAG	AAA	AAA	ATC	GTT	GCC	TTC	AAA	798
	Gln	Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	
	255					260				265					
50	AAC	TGT	ATC	ATT	GCA	GCA	GGC	AGC	CGC	GTA	ACC	AAA	CTG	CCT	840
	Asn	Cys	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	
	270					275				280					

	TTC ATT CCT GAA GAT CCG CGC ATC ATC GAT TCC AGC GGC GCA	882
	Phe Ile Pro Glu Asp Pro Arg Ile Ile Asp Ser Ser Gly Ala	
	285	290
5	TTG GCT CTG AAA GAA GTA CCG GGC AAA CTG CTG ATT ATC GGC	924
	Leu Ala Leu Lys Glu Val Pro Gly Lys Leu Leu Ile Ile Gly	
	295	300
	305	
10	GGC GGC ATT ATC GGC CTC GAG ATG GGT ACG GTT TAC AGC ACG	966
	Gly Gly Ile Ile Gly Leu Glu Met Gly Thr Val Tyr Ser Thr	
	310	315
	320	
15	CTG GGT TCG CGT TTG GAT GTG GTT GAA ATG ATG GAC GGC CTG	1008
	Leu Gly Ser Arg Leu Asp Val Val Glu Met Met Asp Gly Leu	
	325	330
	335	
20	ATG CAA GGC GCA GAC CGC GAT TTG GTA AAA GTA TGG CAA AAA	1050
	Met Gln Gly Ala Asp Arg Asp Leu Val Lys Val Trp Gln Lys	
	340	345
	350	
	CAA AAC GAA TAC CGT TTT GAC AAC ATT ATG GTC AAC ACC AAA	1092
	Gln Asn Glu Tyr Arg Phe Asp Asn Ile Met Val Asn Thr Lys	
	355	360
25	ACC GTT GCA GTT GAG CCG AAA GAA GAC GGC GTT TAC GTT ACC	1134
	Thr Val Ala Val Glu Pro Lys Glu Asp Gly Val Tyr Val Thr	
	365	370
	375	
30	TTT GAA GGC GCG AAC GCC CCT AAA GAG CCG CAA CGC TAC GAT	1176
	Phe Glu Gly Ala Asn Ala Pro Lys Glu Pro Gln Arg Tyr Asp	
	380	385
	390	
35	GCC GTA TTG GTT GCC GCC GGC CGC GCG CCC AAC GGC AAA CTC	1218
	Ala Val Leu Val Ala Ala Gly Arg Ala Pro Asn Gly Lys Leu	
	395	400
	405	
40	ATC AGC GCG GAA AAA GCA GGC GTT GCC GTA ACC GAT CGC GGC	1260
	Ile Ser Ala Glu Lys Ala Gly Val Ala Val Thr Asp Arg Gly	
	410	415
	420	
	TTC ATC GAA GTG GAC AAA CAA ATG CGT ACC AAT GTG CCG CAC	1302
	Phe Ile Glu Val Asp Lys Gln Met Arg Thr Asn Val Pro His	
	425	430
45	ATC TAC GCC ATC GGC GAC ATC GTC GGT CAG CCG ATG TTG GCG	1344
	Ile Tyr Ala Ile Gly Asp Ile Val Gly Gln Pro Met Leu Ala	
	435	440
	445	
50	CAC AAA GCC GTT CAC GAA GGC CAC GTT GCC GCC GAA AAC TGC	1386
	His Lys Ala Val His Glu Gly His Val Ala Ala Glu Asn Cys	
	450	455
	460	

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12	GCC GGC AAC AAA GCC TAC TTC GAC GCA CGG GTG ATT CCG GGC	1428
	Ala Gly Asn Lys Ala Tyr Phe Asp Ala Arg Val Ile Pro Gly	
	465 470 475	
5	GTT GCC TAC ACT TCC CCC GAA GTG GCG TGG GTG GGC GAA ACC	1470
	Val Ala Tyr Thr Ser Pro Glu Val Ala Trp Val Gly Glu Thr	
	480 485 490	
10	GAA CTG TCC GCC AAA GCC TCC GCG CGC AAA ATC ACC AAA GCC	1512
	Glu Leu Ser Ala Lys Ala Ser Ala Arg Lys Ile Thr Lys Ala	
	495 500	
15	AAC TTC CCG TGG GCG GCT TCC GGC CGT GCG ATT GCC AAC GGT	1554
	Asn Phe Pro Trp Ala Ala Ser Gly Arg Ala Ile Ala Asn Gly	
	505 510 515	
20	TGC GAC AAG CCG TTT ACC AAG CTG ATT TTT GAT GCC GAA ACC	1596
	Cys Asp Lys Pro Phe Thr Lys Leu Ile Phe Asp Ala Glu Thr	
	520 525 530	
	GGC CGC ATC ATC GGC GGC ATT GTC GGT CCG AAC GGT GGC	1638
	Gly Arg Ile Ile Gly Gly Ile Val Gly Pro Asn Gly Gly	
	535 540 545	
25	GAT ATG ATC GCG AAG TCT GCC TTG CCA TCG AAA TGG GCT GCG	1680
	Asp Met Ile Ala Lys Ser Ala Leu Pro Ser Lys Trp Ala Ala	
	550 555 560	
30	ACA CGT GCA GAC ATC GGC AAA ACC ATC CAC CCG CGC CCG ACC	1722
	Thr Arg Ala Asp Ile Gly Lys Thr Ile His Pro Arg Pro Thr	
	565 570	
35	TTG GGC GAA TCC ATC GGT ATG GCG GCG GAA GTG GCA TTG GGT	1764
	Leu Gly Glu Ser Ile Gly Met Ala Ala Glu Val Ala Leu Gly	
	575 580 585	
40	ACT TGT ACC GAC CTG CCT CCG CAA AAG AAA AAA TAA	1800
	Thr Cys Thr Asp Leu Pro Pro Gln Lys Lys Lys *	
	590 595 599	
	ATCC GACTGAATAA ACAGCCGATA AGGT TTATTT GA	1836
45	SEQ ID NO: 2	
	SEQUENCE TYPE : Nucleotide	
	SEQUENCE LENGTH: 15 bases	
50	ATGCTAGATA AAAGA	15

SEQ ID NO: 3  
SEQUENCE TYPE : Amino acid  
SEQUENCE LENGTH: 25 amino acids  
MOLECULE TYPE: Sequence N-terminal of P64k protein from outer membrane of *N. meningitidis*

15 Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp  
 1 5 10 15  
 Ile Gly Gly His Glu Asn Val Asp Ile Ile  
 20 25

20           SEQ ID NO: 4  
SEQUENCE TYPE : Nucleotide  
SEQUENCE LENGTH: 12 bases  
25           CTAGATAAAA GA           12

30 SEQ ID NO: 5  
SEQUENCE TYPE : Nucleotide  
SEQUENCE LENGTH: 8 bases

35 TCTTTTAT 8

SEQ ID NO: 6  
SEQUENCE TYPE : Amino acid  
SEQUENCE LENGTH: 221 amino acids  
MOLECULE TYPE: Sequence which includes variable regions of P1.15 protein

```

45   Leu Gln Leu Thr Glu Pro Pro Ser Lys Ser Gln Pro Gln Val Lys
      1           5           10          15

      Val Thr Lys Ala Lys Ser Arg Ile Arg Thr Gln Ile Ser Asp Phe
      20          25          30

50   Gly Ser Phe Ile Gly Phe Lys Gly Ser Glu Asp Leu Gly Glu Gly
      35          40          45

      Leu Lys Ala Val Trp Gln Leu Glu Gln Asp Val Ser Val Ala Gly
      50          55          60

```

Gly Gly Ala Thr Gln Trp Gly Asn Arg Glu Ser Phe Val Gly Leu  
 65 70 75

5 Ala Gly Glu Phe Gly Thr Leu Arg Ala Gly Arg Val Ala Asn Gln  
 80 85 90

10 Phe Asp Asp Ala Ser Gln Ala Ile Asp Pro Trp Asp Ser Asn Asn  
 95 100 105

15 Asp Val Ala Ala Ser Gln Leu Gly Ile Phe Lys Arg His Asp Asp  
 110 115 120

20 Met Pro Val Ser Val Arg Tyr Asp Ser Pro Asp Phe Ser Gly Phe  
 125 130 135

25 Ser Gly Ser Val Gln Phe Val Pro Ile Gln Asn Ser Lys Ser Ala  
 140 145 150

30 Tyr Thr Pro Ala Tyr His Tyr Thr Arg Gln Asn Asn Ala Asp Val  
 155 160 165

35 Phe Val Pro Ala Val Val Gly Lys Pro Gly Ser Asp Val Tyr Val  
 170 175 180

40 Ala Gly Leu Asn Tyr Lys Asn Gly Gly Phe Ala Gly Ser Tyr Ala  
 185 190 195

45 Phe Lys Tyr Ala Arg His Ala Asn Val Gly Arg Asn Ala Phe Glu  
 200 205 210

50 Leu Phe Leu Leu Gly Ser Thr Ser Asp Glu Ala  
 215 220

55 SEQ ID NO: 7  
 SEQUENCE TYPE : Amino acid  
 60 SEQUENCE LENGTH: 6 amino acids  
 MOLECULE TYPE: Sequence corresponding to the fusion site  
 between N-terminal of P64k and P1.15

65 Gly Asp Ala Leu Gln Leu  
 1 5

SEQ ID NO: 8  
SEQUENCE TYPE : Nucleotide  
SEQUENCE LENGTH: 19 bases  
5 MOLECULE TYPE: Sequence corresponding to the fusion of  
N-terminal from gene M-6 and from gene P1.15  
  
10 GGCGACGCGC TGCAGTTGA 19  
  
SEQ ID NO: 9  
SEQUENCE TYPE : Amino acid  
15 SEQUENCE LENGTH: 6 amino acids  
MOLECULE TYPE: Sequence corresponding to the fusion site  
between C-terminal of P64k and P1.15  
20  
Glu Ala Asn Ala Tyr Glu  
1 5  
  
25 SEQ ID NO: 10  
SEQUENCE TYPE : Nucleotide  
SEQUENCE LENGTH: 18 bases  
30 MOLECULE TYPE: Sequence corresponding to the fusion of  
C-terminal from gene M-6 and from gene P1.15  
  
GAAGCCAACG CGTACGAA 18  
35  
SEQ ID NO: 11  
SEQUENCE TYPE : Amino acid  
40 SEQUENCE LENGTH: 111 amino acids  
MOLECULE TYPE: p64k N-terminal comprising homology region  
with "lypoil binding site" from E. coli Acetyl transferase  
  
45 Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile Gly Gly His Glu  
1 5 10 15  
Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly Asp Thr Ile  
50 20 25 30  
Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp Lys Ala Thr  
35 40 45  
55

	Met Asp Val Pro Ala Glu Val Ala Gly Val Val Lys Glu Val Lys
	50 55 60
5	Val Lys Val Gly Asp Lys Ile Ser Glu Gly Gly Leu Ile Val Val
	65 70 75
	Val Glu Ala Glu Gly Thr Ala Ala Ala Pro Lys Ala Glu Ser Ala
	80 85 90
10	Ala Ala Pro Arg Lys Lys Pro Leu Lys Cys Arg Trp Val Pro Gln
	95 100 105
	Ala Ala Gln Phe Gly Gly
15	110

SEQ ID NO: 12

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 112 amino acids

MOLECULE TYPE: "lypoil binding site" from E. coli Acetyl-transferase

25	Val Lys Glu Val Asn Val Pro Asp Ile Gly Gly Asp Glu Val Glu
	1 5 10 15
30	Val Thr Glu Val Met Val Lys Val Gly Asp Lys Val Ala Ala Glu
	20 25 30
	Gln Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val
	35 40 45
35	Pro Ala Pro Phe Ala Gly Val Val Lys Glu Leu Lys Val Asn Val
	50 55 60
	Gly Asp Lys Val Lys Thr Gly Ser Leu Ile Met Ile Phe Glu Val
40	65 70 75
	Glu Gly Ala Ala Pro Ala Ala Ala Pro Ala Lys Gln Glu Ala Ala
	80 85 90
45	Ala Pro Ala Pro Ala Ala Lys Ala Glu Ala Pro Ala Ala Ala Pro
	95 100 105
	Ala Ala Lys Ala Glu Gly Lys
	110

50

55

SEQ ID NO: 13

5 SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 481 amino acids

MOLECULE TYPE: P64k fragment comprising the homology region  
10 with Lipoamide Dehydrogenase from E. coli

Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	Val	Leu	Gly	Gly	Gly	Pro
1										10				15

Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Asp	Glu	Gly	Leu	Lys
										20	25			30

Val	Ala	Ile	Val	Glu	Arg	Tyr	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu
									35	40			45	

Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala
								50	55			60		

Val	Ile	Asp	Glu	Val	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr
						65				70			75	

Pro	Glu	Pro	Ala	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp
						80			85			90		

Gly	Val	Val	Ser	Arg	Leu	Thr	Gly	Phe	Gly	Arg	Tyr	Gly	Glu	Lys
					95				100				105	

Arg	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro
					110				115				120	

His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	Gln
					125				130			135		

Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	Asn	Cys
						140			145				150	

Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	Phe	Ile	Pro
						155			160			165		

Glu	Asp	Pro	Arg	Ile	Ile	Asp	Ser	Ser	Gly	Ala	Leu	Ala	Leu	Lys
						170			175			180		

Glu	Val	Pro	Gly	Lys	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Ile	Ile	Gly
						185			190			195		

Leu	Glu	Met	Gly	Thr	Val	Tyr	Ser	Thr	Leu	Gly	Ser	Arg	Leu	Asp
						200			205			210		

Val	Val	Glu	Met	Met	Asp	Gly	Leu	Met	Gln	Gly	Ala	Asp	Arg	Asp
						215			220			225		

	Leu	Val	Lys	Val	Trp	Gln	Lys	Gln	Asn	Glu	Tyr	Arg	Phe	Asp	Asn
5					230					235					240
	Ile	Met	Val	Asn	Thr	Lys	Thr	Val	Ala	Val	Glu	Pro	Lys	Glu	Asp
					245					250					255
10	Gly	Val	Tyr	Val	Thr	Phe	Glu	Gly	Ala	Asn	Pro	Pro	Lys	Glu	Pro
					260					265					270
	Gln	Arg	Tyr	Asp	Ala	Val	Leu	Val	Ala	Ala	Gly	Arg	Ala	Pro	Asn
					275					280					285
15	Gly	Lys	Leu	Ile	Ser	Ala	Glu	Lys	Ala	Gly	Val	Ala	Val	Thr	Asp
					290					295					300
20	Arg	Gly	Phe	Ile	Glu	Val	Asp	Lys	Gln	Met	Arg	Thr	Asn	Val	Pro
					305					310					315
	His	Ile	Tyr	Ala	Ile	Gly	Asp	Ile	Val	Gly	Gln	Pro	Met	Leu	Ala
					320					325					330
25	His	Lys	Ala	Val	His	Glu	Gly	His	Val	Ala	Ala	Glu	Asn	Cys	Ala
					335					340					345
	Gly	Thr	Lys	Ala	Tyr	Phe	Asp	Ala	Ala	Val	Ile	Pro	Gly	Val	Ala
					350					355					360
30	Tyr	Thr	Ser	Pro	Glu	Val	Ala	Trp	Val	Gly	Glu	Thr	Glu	Leu	Ser
					365					370					375
35	Ala	Lys	Arg	Pro	Ala	Gly	Lys	Ile	Thr	Lys	Ala	Asn	Phe	Pro	Trp
					380					385					390
	Ala	Ala	Ser	Gly	Arg	Ala	Ile	Ala	Asn	Gly	Cys	Asp	Lys	Pro	Phe
					395					400					405
40	Thr	Lys	Leu	Ile	Phe	Asp	Ala	Glu	Thr	Gly	Arg	Ile	Ile	Gly	Gly
					410					415					420
	Gly	Ile	Val	Gly	Pro	Asn	Gly	Gly	Asp	Met	Ile	Ala	Lys	Ser	Ala
					425					430					435
45	Leu	Pro	Ser	Lys	Leu	Gly	Cys	Asp	Ala	Ala	Asp	Val	Gly	Lys	Thr
					440					445					450
50	Ile	His	Pro	Arg	Pro	Thr	Leu	Gly	Glu	Ser	Ile	Gly	Met	Ala	Ala
					455					460					465
	Glu	Val	Ala	Leu	Gly	Thr	Cys	Thr	Asp	Leu	Pro	Pro	Gln	Lys	Lys
					470					475					480
55	Lys														

SEQ ID NO: 14  
 5 SEQUENCE TYPE : Amino acid  
 SEQUENCE LENGTH: 472 bases  
 MOLECULE TYPE: Segment of E. coli Lipoamide Dehydrogenase  
 10 with homology to P64k protein

Ser	Thr	Glu	Ile	Lys	Thr	Gln	Val	Val	Val	Leu	Gly	Ala	Gly	Pro
1					5					10				15
Ala	Gly	Tyr	Ser	Ala	Ala	Phe	Arg	Cys	Ala	Asp	Leu	Gly	Leu	Glu
	20								25					30
Thr	Val	Ile	Val	Glu	Arg	Tyr	Asn	Thr	Leu	Gly	Gly	Val	Cys	Leu
				35					40					45
Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Val	Ala	Lys
				50					55					60
Val	Ile	Glu	Glu	Ala	Lys	Ala	Leu	Ala	Glu	His	Gly	Ile	Val	Phe
25		65							70	.				75
Gly	Glu	Pro	Lys	Thr	Asp	Ile	Asp	Lys	Ile	Thr	Trp	Lys	Glu	Lys
		80							85					90
Val	Ile	Asn	Gln	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Gly
30				95					100					105
Arg	Lys	Val	Lys	Val	Val	Asn	Gly	Leu	Gly	Lys	Phe	Thr	Gly	Ala
				110					115					120
Asn	Thr	Leu	Glu	Val	Glu	Gly	Glu	Asn	Gly	Lys	Thr	Val	Ile	Asn
				125				130						135
Phe	Asp	Asn	Ala	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Pro	Ile	Gln	Leu
40				140					145					150
Pro	Phe	Ile	Pro	His	Glu	Asp	Pro	Arg	Ile	Trp	Asp	Ser	Thr	Asp
				155				160						165
Ala	Leu	Glu	Leu	Lys	Glu	Val	Pro	Glu	Arg	Leu	Leu	Val	Met	Gly
45				170					175					180
Gly	Gly	Ile	Ile	Gly	Leu	Glu	Met	Gly	Thr	Val	Tyr	His	Ala	Leu
				185				190						195
Gly	Ser	Gln	Ile	Asp	Val	Val	Glu	Met	Phe	Asp	Gln	Val	Ile	Pro
				200					205					210
Ala	Ala	Asp	Lys	Asp	Ile	Val	Lys	Val	Phe	Thr	Lys	Arg	Ile	Ser
55				215					220					225

Lys Lys Phe Asn Leu Met Leu Glu Thr Lys Val Thr Ala Val Glu  
 5 230 235 240

Ala Lys Glu Asp Gly Ile Tyr Val Thr Met Glu Gly Lys Lys Ala  
 10 245 250 255

Pro Ala Glu Pro Gln Arg Tyr Asp Ala Val Leu Val Ala Ile Gly  
 15 260 265 270

Arg Val Pro Asn Gly Lys Asn Leu Asp Ala Gly Lys Ala Gly Val  
 20 275 280 285

Glu Val Asp Asp Arg Gly Phe Ile Arg Val Asp Lys Gln Leu Arg  
 25 290 295 300

Thr Asn Val Pro His Ile Phe Ala Ile Gly Asp Ile Val Gly Gln  
 30 305 310 315

Pro Met Leu Ala His Lys Gly Val His Glu Gly His Val Ala Ala  
 35 320 325 330

Glu Val Ile Ala Gly Lys Lys His Tyr Phe Asp Pro Lys Val Ile  
 40 335 340 345

Pro Ser Ile Ala Tyr Thr Glu Pro Glu Val Ala Trp Val Gly Leu  
 45 350 355 360

Thr Glu Lys Glu Ala Lys Glu Lys Gly Ile Ser Tyr Glu Thr Ala  
 50 365 370 375

Thr Phe Pro Trp Ala Ala Ser Gly Arg Ala Ile Ala Ser Asp Cys  
 55 380 385 390

Ala Asp Gly Met Thr Lys Leu Ile Phe Asp Lys Glu Ser His Arg  
 60 395 400 405

Val Ile Gly Gly Ala Ile Val Gly Thr Asn Gly Gly Glu Leu Leu  
 65 410 415 420

Gly Glu Ile Gly Leu Ala Ile Glu Met Gly Cys Asp Ala Glu Asp  
 70 425 430 435

Ile Ala Leu Thr Ile His Ala His Pro Thr Leu His Glu Ser Val  
 75 440 445 450

Gly Leu Ala Ala Glu Val Phe Glu Gly Ser Ile Thr Asp Leu Pro  
 80 455 460 465

Asn Pro Lys Ala Lys Lys Lys  
 85 470

## **Claims**

1. A recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of *Neisseria*

meningitidis, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.

2. A recombinant polynucleotide according to claim 1, wherein said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1.

- 5       3. A recombinant polynucleotide according to claim 1 or 2, further comprising a nucleotide sequence of a cloning or expression vector.

- 10      4. A transformed microorganism, containing a recombinant polynucleotide according to any of claims 1 to 3.

- 15      5. A transformed microorganism according to claim 4, which is capable of expressing the protein P64k of *N. meningitidis*.

- 15      6. A transformed microorganism according to claim 5, which is an *Escherichia coli* strain, e.g. *E. coli* strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of *N. meningitidis*, e.g. the expression vector pM-6.

- 20      7. A recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of *N. meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.

- 25      8. A recombinant proteinaceous substance according to claim 7, which is a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of *N. meningitidis*.

9. A vaccine composition, comprising a recombinant protein according to claim 7 or 8, together with a suitable carrier, diluent or adjuvant.

- 30      10. A vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of *N. meningitidis*, together with a suitable carrier, diluent or adjuvant.

- 35      11. Monoclonal antibody, raised against a recombinant proteinaceous substance according to claim 7 or 8, or against a lipoamide dehydrogenase or acetyl transferase, and capable of binding a protein P64k of *N. meningitidis*.

- 40      12. A process for preparing a protein P64k of *Neisseria meningitidis*, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.

- 45      13. A method for the isolation and expression of a gene which codes for a protein belonging to the outer membrane of *N. meningitidis* and its use in vaccine preparations, wherein the gene from the strain of *N. meningitidis* B:4:P1.15, identified as M-6, is obtained from the screening of a genomic library in the EMBL 3, and is cloned and expressed in a suitable host, coding for a protein of 64kDa belonging to the outer membrane of *N. meningitidis* which has bactericidal activity against different serogroups, serotypes and subtypes of *N. meningitidis*.

- 50      14. A nucleotide sequence obtained by the method of claim 13, characterized in that the sequence is corresponding with the M-6 gene and codes for the P64k protein, identified in the sequence listing with number 1.

- 55      15. A recombinant DNA according to claims 13 and 14, characterized in that it is a molecule which contains the M-6 gene which codes for P64k protein.

16. A recombinant DNA according to claim 15, characterized in that it is a phage, a plasmid or an expression vector.

17. A recombinant DNA according to claims 15 and 16, characterized in that it is the phage EMBL 3,  
5 plasmid pM-1 and expression vector pM-6.

18. A transformed microorganism according to the preceding claims, characterized in that it results from  
the transformation of a suitable host, carries the M-6 gene, expresses high levels of P64k protein and  
maintains good viability and cellular stability.

10 19. A transformed microorganism according to claim 18, characterized in that it is the clone HBM64 which  
is obtained from the transformation of E. coli host strain HB101 with the expression vector pM-6, and it  
presents high stability and viability and expression levels of P64k protein higher than 25 % of the total  
protein of the cell.

15 20. A recombinant protein obtained according to the preceding claims, characterized in that it essentially  
has the amino acid sequence shown in the sequence listing under SEQ ID NO:1.

20 21. Protein P64k according to preceding claims characterized in that it is the direct result of the expression  
of the M-6 gene as well as any peptide which has important immunological regions obtained by  
chemical synthesis or enzymatic degradation of P64k protein and its use in fusion proteins and  
polysaccharide protein conjugates for monovalent and multivalent vaccine preparations.

25 22. A vaccine preparation comprising protein P64k and at least one carrier, diluent or adjuvant used for  
vaccine preparations, as well as comprising any protein of Lipoamide dehydrogenase or Acetyl  
transferase from other organism or modification thereof, which is able to induce antibodies against the  
P64k protein.

30

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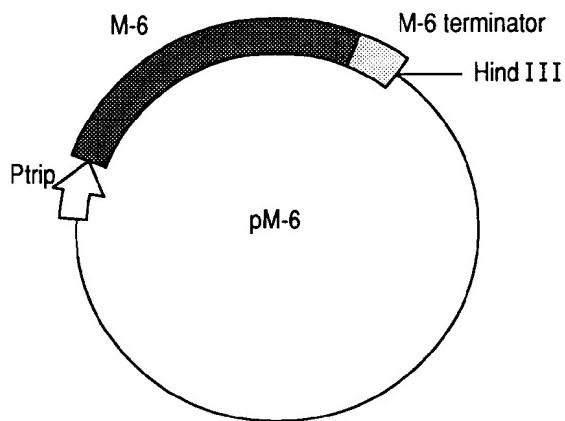


FIG. 1

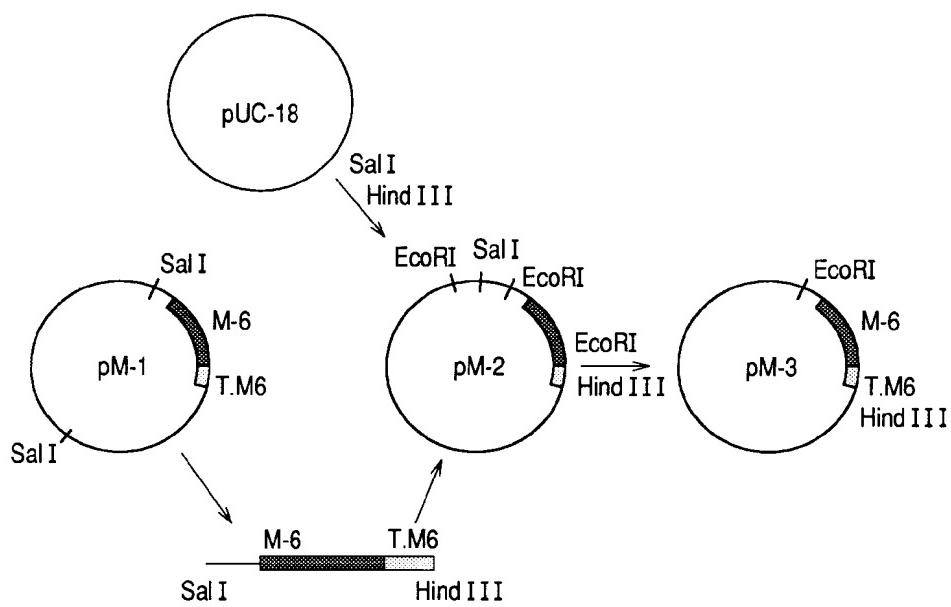


FIG. 2

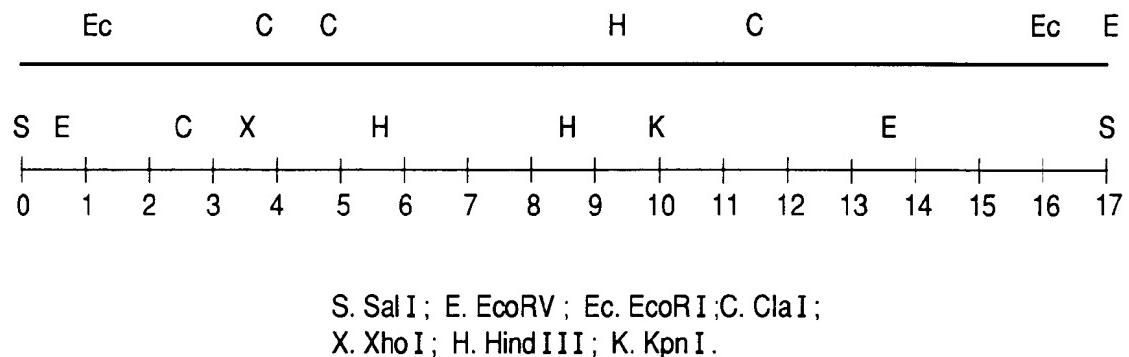


FIG. 3

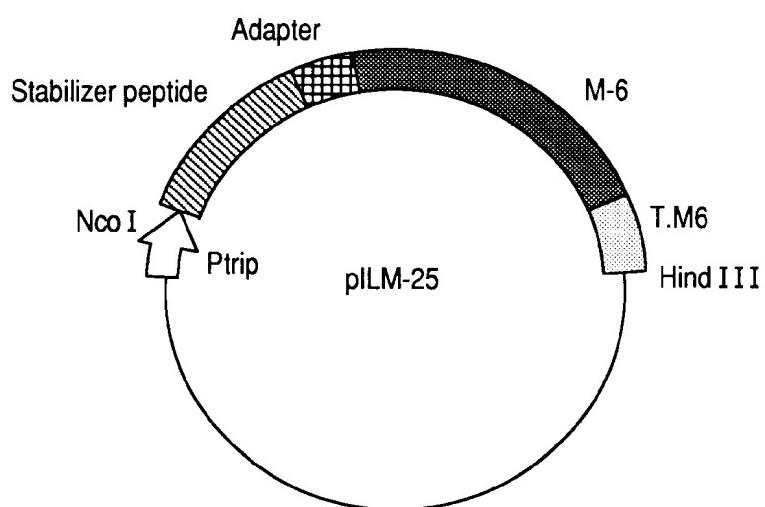


FIG. 4

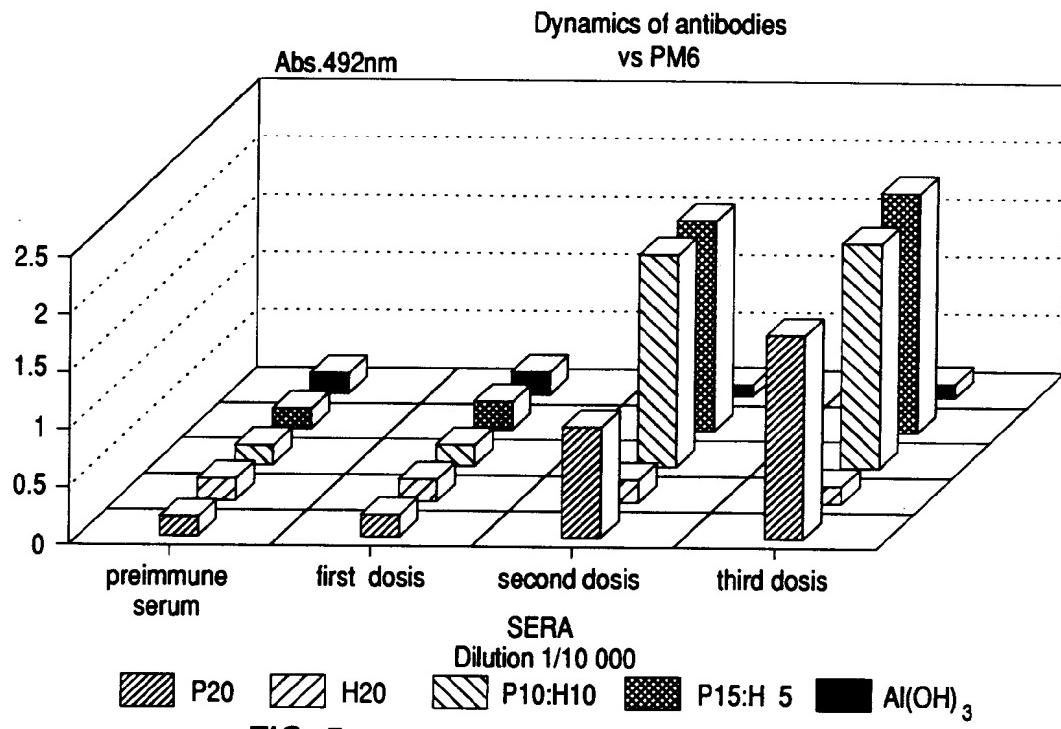


FIG. 5

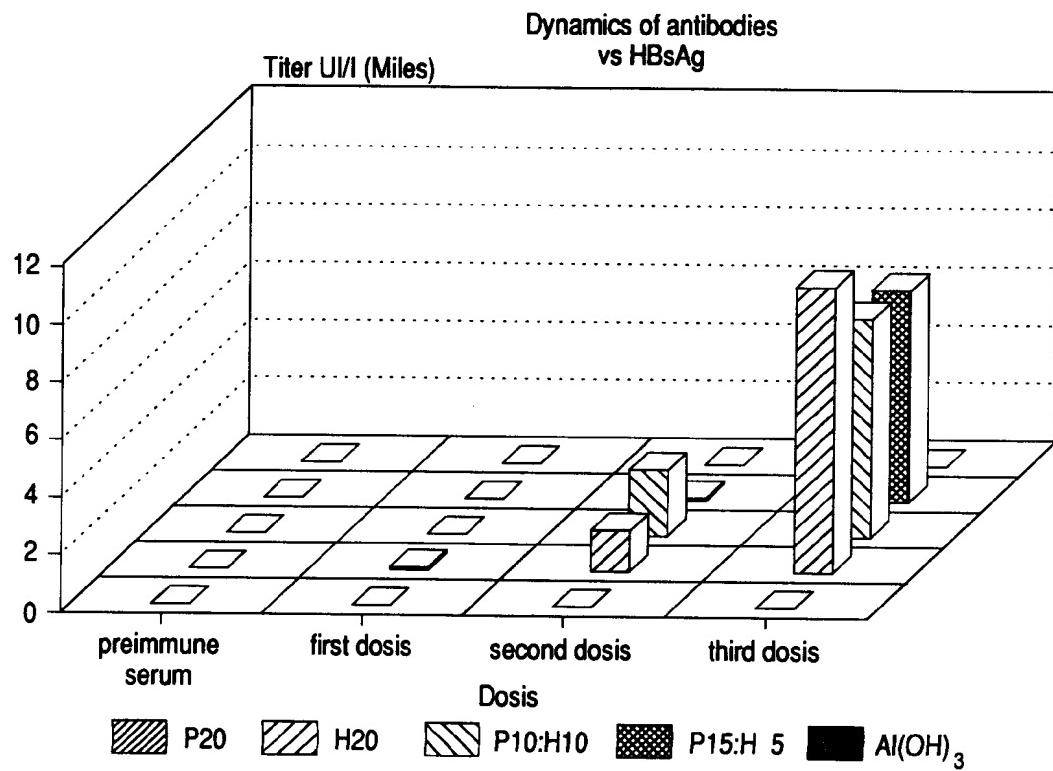


FIG. 6